#4

SEQUENCE LISTING

<110>   TransMIT Gesellschaft für Technologietransfer mbH
        TransMIT Gesellschaft für Technologietransfer mbH

<120>   Method for screening the allelic state at the 5'-flanking region of the
aS1 casein gene

<130>   An127/Pri

<140>   PCT/DE 03/02747
<141>   2003-08-15

<150>   DE 102 38 433 A1
<151>   2002-08-16

<160>   8

<170>   PatentIn version 3.1

<210>   1
<211>   18
<212>   DNA
<213>   Bos spec.

<220>
<221>   Primer 2
<222>   (1)..(18)
<223>   18 basepair, single stranded nucleic acid (linear)

<400>   1
gaagaagcag caagctgg   18

<210>   2
<211>   19
<212>   DNA
<213>   Bos spec.

<220>
<221>   Primer 3
<222>   (1)..(19)
<223>   19 basepair, single stranded nucleic acid (linear)

<400>   2
ccttgaaata ttctaccag   19

<210>   3
<211>   1061
<212>   DNA
<213>   Bos taurus

<220>
<221>   alpha-S1Kaseingen

<400>   3

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gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa     120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg     180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt     240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat     300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa     360

taaccataaa tctagggttt tgttggggtt ttttttttgtt tgttaatttta gaacaatgcc     420

attccatttc ctgtataatg agtcacttct ttgttgtaaa ctctccttag aatttcttgg     480

gagaggaact gaacagaaca ttgatttcct atgtgagaga attcttagaa tttaaataaa     540

cctgttggtt aaactgaaac cacaaaatta gcattttact aatcagtagg tttaaatagc     600

ttggaagcaa aagtctgcca tcaccttgat catcaaccca gcttgctgct tcttcccagt     660

cttgggttca aggtattatg tatacatata acaaaatttc tatgattttc ctctgtctca     720

tctttcattc ttcactaata cgcagttgta acttttctat gtgattgcaa gtattggtac     780

tttcctatga tatactgtta gcttaaaaat atatttgcaa atgttgatac tatctatctc     840

agagctatag gtgaaaaatt aaatactttt ataaagacca aattgatcat ttttaaacga     900

aattcttata tactgaaaat gtagatacat aacttcagta tagatttatg gtaaaataat     960

ttgaatcatt tttgtcaaat tctgtaaaaa gttgtcatac agaataattt ataatatttt    1020

tgttttcata gaaataacat ttctggtaga atatttcaag g                        1061
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<210> 4
<211> 652
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region from position 616 and Exon 1 at position 617
<222> (1)..(652)
<223> Mutation/SNP position 83 (A to G), position 98 (A to G), position 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1 -bindingsite), position 541 (G to A); deletion TT between position 389 and 394 compaired with Allel2

<400> 4
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aagtttatac aataattgta ttttcttttt gcaggaaaaa   120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg   180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt   240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcct ttacaggtat   300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa   360

taaccataaa tctagggttt tgttggggtt ttttgtttgt taatttagaa caatgccatt   420

ccatttcctg tataatgagt cgcttctttg ttgtaaactc tccttagaat ttcttgggag   480

aggaactgaa cagaacattg atttcctatg tgagagaatt cttagaattt aaataaacct   540

attggttaaa ctgaaaccac aaaattagca ttttactaat cagtaggttt aaatagcttg   600

gaagcaaaag tctgccatca ccttgatcat caacccagct tgctgctttc tt   652

<210> 5
<211> 654
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region and Exon 1
<222> (1)..(654)
<223> Bindingsite for transcriptionfactor AP-1 at position 438 to 445
Bindingsite for transcriptionfactor YY-1 at position 443 to 448

<400> 5
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa   120

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gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg        180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt        240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat        300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa        360

taaccataaa tctagggttt tgttgggggtt ttttttgttt gttaatttag aacaatgcca      420

ttccatttcc tgtataatga gtcacttctt tgttgtaaac tctccttaga atttcttggg       480

agaggaactg aacagaacat tgatttccta tgtgagagaa ttcttagaat ttaaataaac       540

ctgttggtta aactgaaacc acaaaattag cattttacta atcagtaggt ttaaatagct       600

tggaagcaaa agtctgccat caccttgatc atcaacccag cttgctgctt tctt            654


<210>   6
<211>   650
<212>   DNA
<213>   Bos taurus

<220>
<221>   CSN1S1-gene, 5`flanking region
<222>   (1)..(650)
<223>   Bindingsite for transcriptionfactor AP-1 at position 434 to 441
        Bindingsite for transcriptionfactor YY-1 at position 439 to 444
        deletion G and TTT between 390 and 396 compaired with  Allel 2


<400>   6
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg         60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa       120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg        180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt        240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat        300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa        360

taaccataaa tctagggttt tgttggggtt ttttttgtta atttagaaca atgccattcc       420

atttcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagag       480

gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt       540

tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga       600

agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt                  650
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<210> 7
<211> 650
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region
<222> (1)..(650)
<223> Bindingsite for transcriptionfactors: AP-1 at position 434 to 441
     , ABF1 at position 469 to 483, YY-1 at position 439 to 444;
     mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
     gsite;
     deletion G and TTT between position 390 and 396 compaired with Al
     lel 2

<400> 7
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa   120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg   180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt   240

aataaaaatt gaaaaatttt gaagaccca ttttgtccca agaatttcat ttacaggtat   300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa   360

taaccataaa tctagggttt tgttggggtt ttttttgtta atttagaaca atgccattcc   420

atttcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagac   480

gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt   540

tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga   600

agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt   650

<210> 8
<211> 20
<212> DNA
<213> Bos spec.

<220>
<221> Primer1
<222> (1)..(20)
<223> 20 basepair, single stranded nucleic acid (linear)

<400> 8
gaatgaatga actagttacc   20